



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 08:39 PM UTC

PDB ID : 9AX8 / pdb_00009ax8
EMDB ID : EMD-43930
Title : 70S initiation complex (tRNA-fMet M1, initiation factor 2 + CUG start codon)
Authors : Mattingly, J.M.; Nguyen, H.A.; Dunham, C.M.
Deposited on : 2024-03-06
Resolution : 2.60 Å(reported)
Based on initial model : 6O9K

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

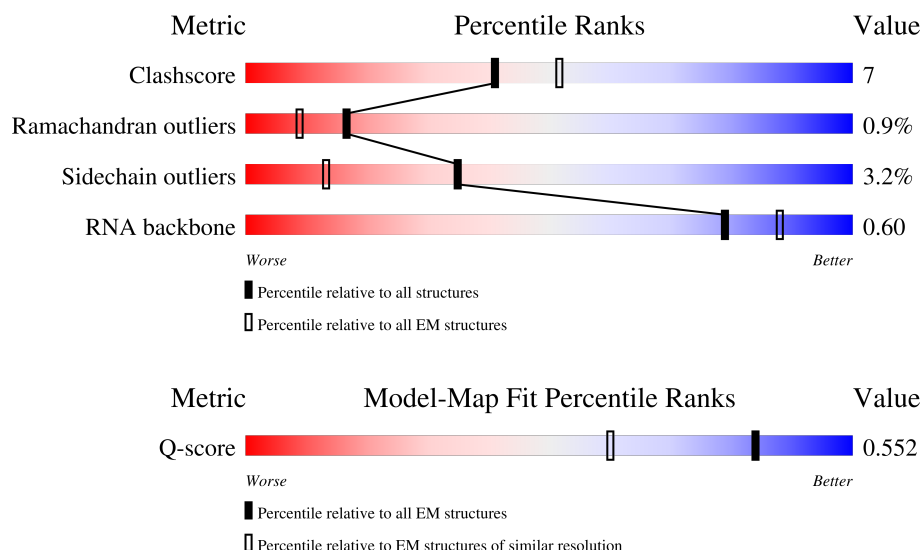
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8728 (2.10 - 3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	79	
2	1	77	
3	2	63	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	3	58	
5	4	209	
6	5	56	
7	6	50	
8	7	46	
9	8	64	
10	9	271	
11	E	201	
12	F	177	
13	H	176	
14	J	142	
15	K	122	
16	L	143	
17	M	136	
18	N	120	
19	O	116	
20	P	114	
21	Q	117	
22	R	103	
23	S	110	
24	T	93	
25	U	102	
26	V	94	
27	X	118	
28	Y	38	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	a	1539	
30	b	218	
31	c	206	
32	d	205	
33	e	150	
34	f	100	
35	g	151	
36	h	129	
37	i	127	
38	j	98	
39	k	117	
40	l	123	
41	m	114	
42	n	61	
43	o	88	
44	p	82	
45	q	80	
46	r	54	
47	s	79	
48	t	85	
49	u	51	
50	x	27	
51	y	77	
52	z	509	
53	A	2903	

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 145067 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 2 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 3 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 4 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 6 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 7 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	6	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 8 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 9 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 10 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 11 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 12 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	H	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 14 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 15 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 16 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 17 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 18 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 19 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 20 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 21 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 22 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 23 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 24 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 25 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	U	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 26 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 27 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	118	Total	C	N	O	P	0	0
			2526	1126	464	819	117		

- Molecule 28 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 29 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 30 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 31 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 32 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 33 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	150	Total	C	N	O	S	0	0
			1106	687	211	202	6		

- Molecule 34 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 35 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 36 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 37 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 38 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 39 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 40 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 41 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 42 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	61	Total	C	N	O	S	0	0
			500	310	108	80	2		

- Molecule 43 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 44 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 45 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 46 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	r	54	Total	C	N	O	0	0
			445	282	83	80		

- Molecule 47 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	s	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 48 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 49 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	u	51	Total	C	N	O	S	0	0
			426	265	86	74	1		

- Molecule 50 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	x	9	Total	C	N	O	P	0	0
			194	87	37	61	9		

- Molecule 51 is a RNA chain called P-site tRNA-fMet M1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	y	77	Total	C	N	O	P	0	0
			1639	732	297	534	76		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
y	30	C	G	conflict	GB 2260466602
y	40	G	C	conflict	GB 2260466602

- Molecule 52 is a protein called Translation initiation factor IF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	z	509	Total	C	N	O	S	0	0
			3847	2409	675	748	15		

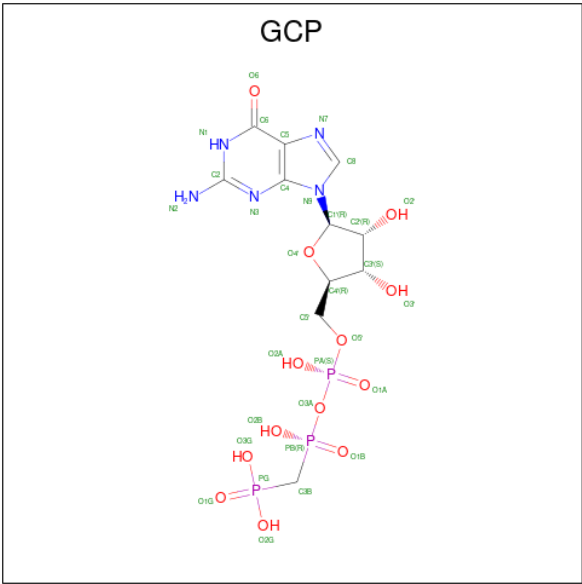
- Molecule 53 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A	2854	Total	C	N	O	P	0	0
			61262	27334	11279	19799	2850		

- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	a	85	Total	Mg	0
			85	85	
54	z	1	Total	Mg	0
			1	1	
54	A	201	Total	Mg	0
			201	201	

- Molecule 55 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

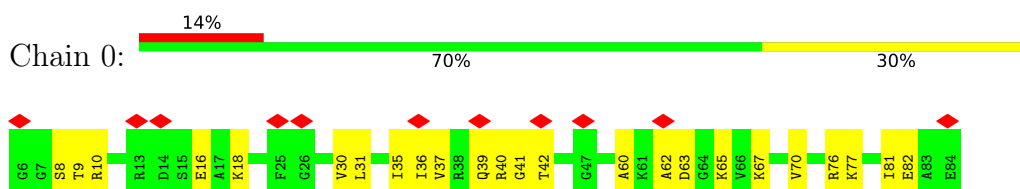


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
55	z	1	32	11	5	13	3	0

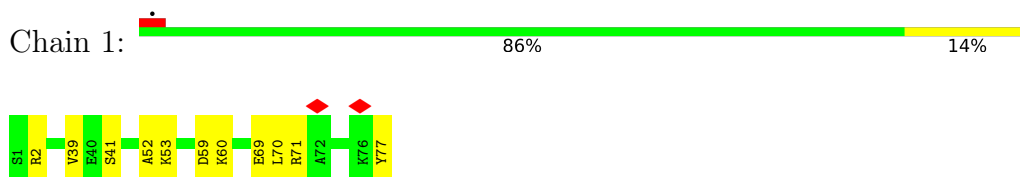
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

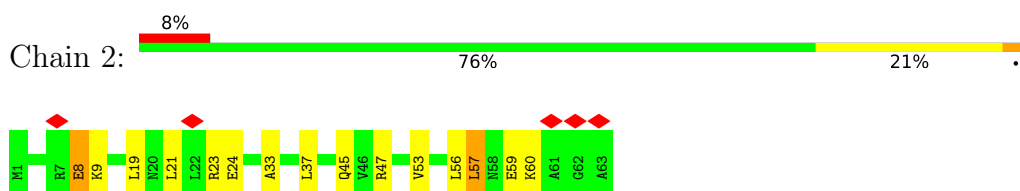
- Molecule 1: 50S ribosomal protein L27



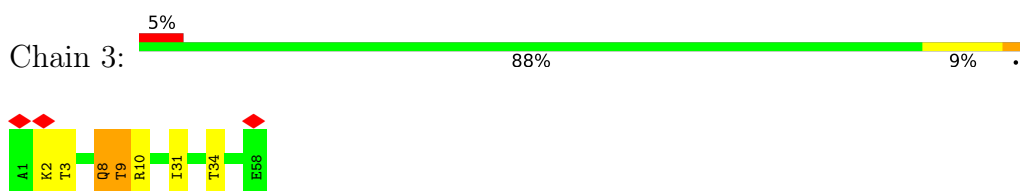
- Molecule 2: 50S ribosomal protein L28



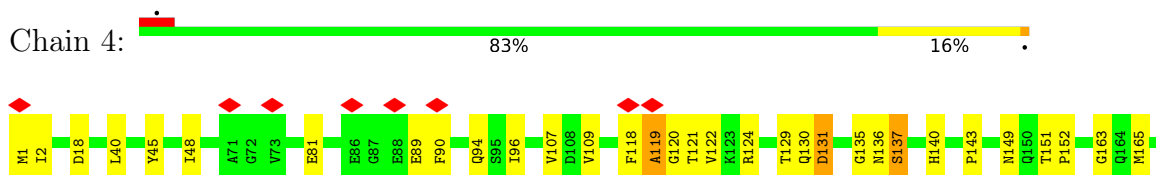
- Molecule 3: 50S ribosomal protein L29

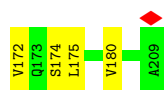


- Molecule 4: 50S ribosomal protein L30

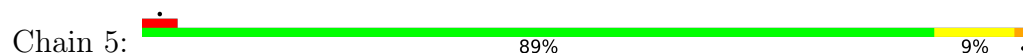


- Molecule 5: 50S ribosomal protein L3





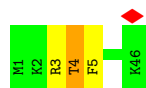
- Molecule 6: 50S ribosomal protein L32



- Molecule 7: 50S ribosomal protein L33



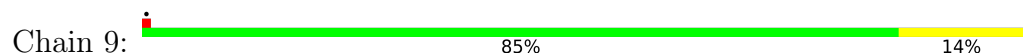
- Molecule 8: 50S ribosomal protein L34



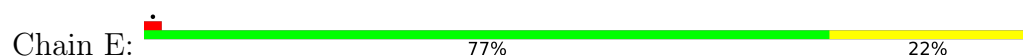
- Molecule 9: 50S ribosomal protein L35

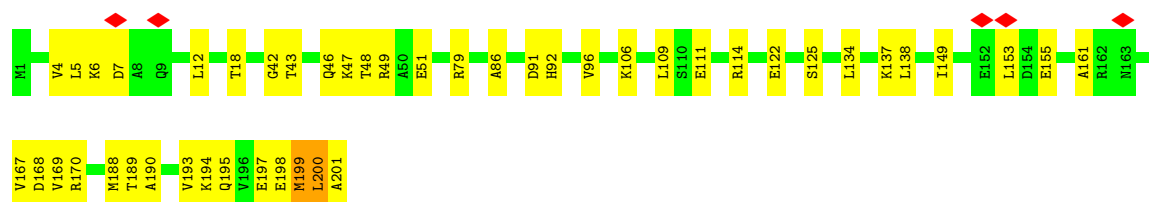


- Molecule 10: 50S ribosomal protein L2

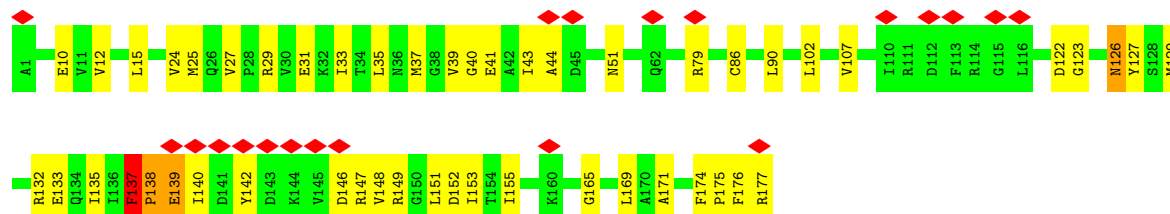


- Molecule 11: 50S ribosomal protein L4

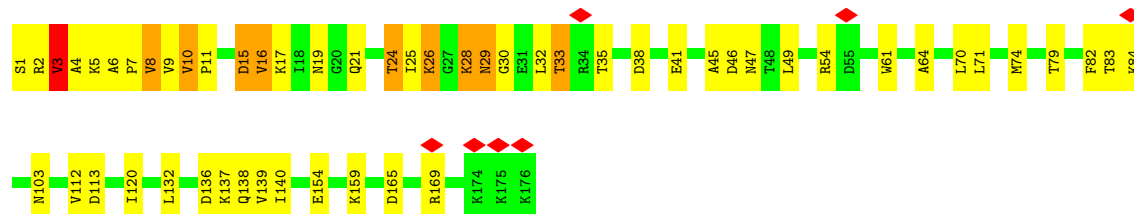




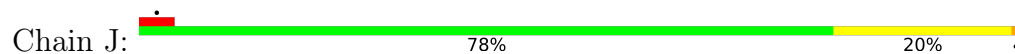
• Molecule 12: 50S ribosomal protein L5



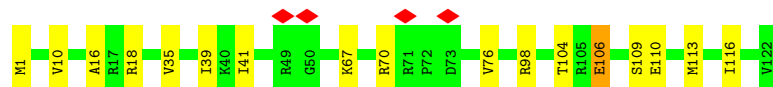
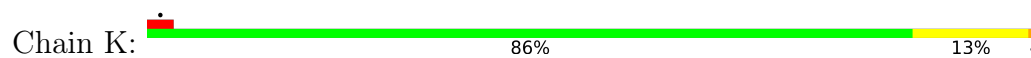
• Molecule 13: 50S ribosomal protein L6



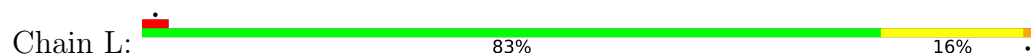
• Molecule 14: 50S ribosomal protein L13

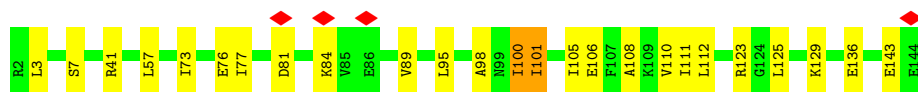


• Molecule 15: 50S ribosomal protein L14

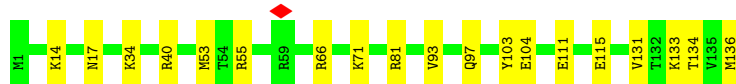
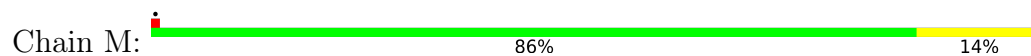


• Molecule 16: 50S ribosomal protein L15

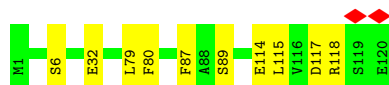




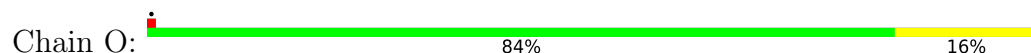
- Molecule 17: 50S ribosomal protein L16



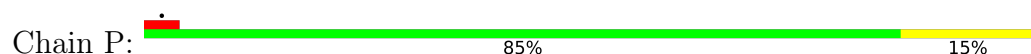
- Molecule 18: 50S ribosomal protein L17



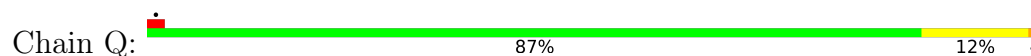
- Molecule 19: 50S ribosomal protein L18



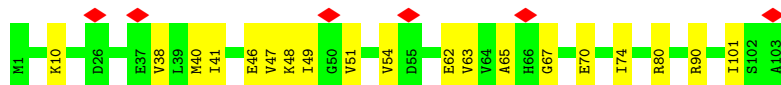
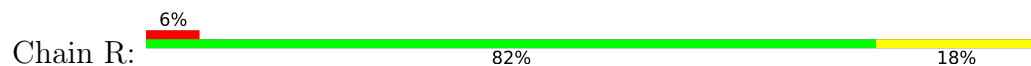
- Molecule 20: 50S ribosomal protein L19



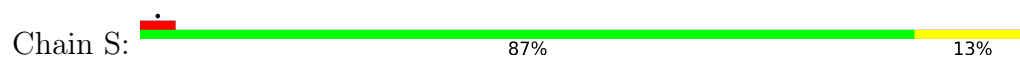
- Molecule 21: 50S ribosomal protein L20



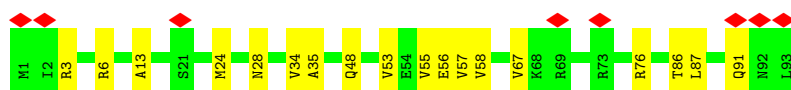
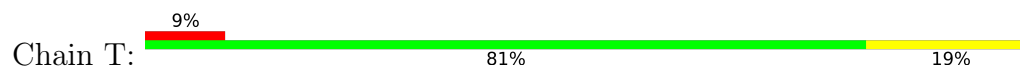
- Molecule 22: 50S ribosomal protein L21



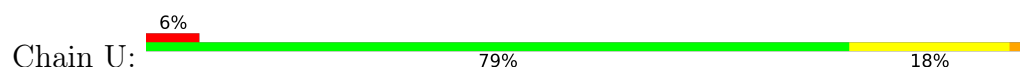
- Molecule 23: 50S ribosomal protein L22



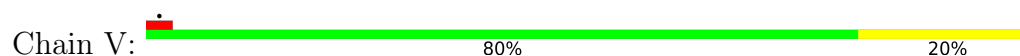
- Molecule 24: 50S ribosomal protein L23



- Molecule 25: 50S ribosomal protein L24



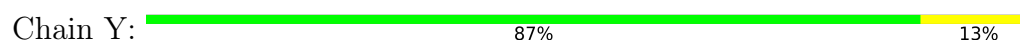
- Molecule 26: 50S ribosomal protein L25



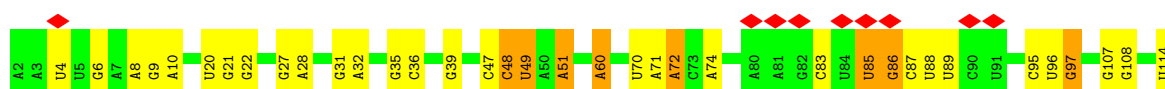
- Molecule 27: 5S ribosomal RNA

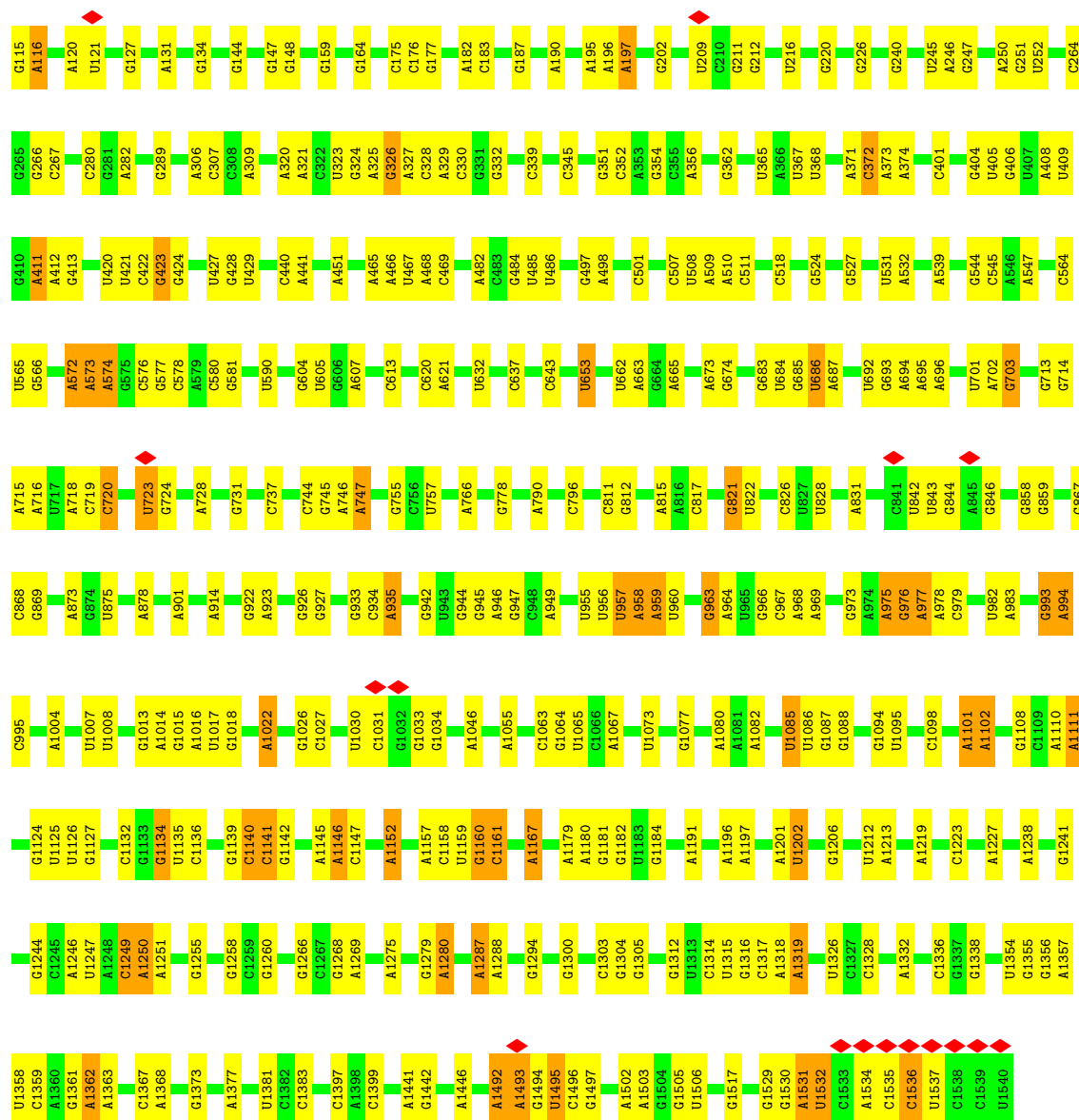


- Molecule 28: 50S ribosomal protein L36

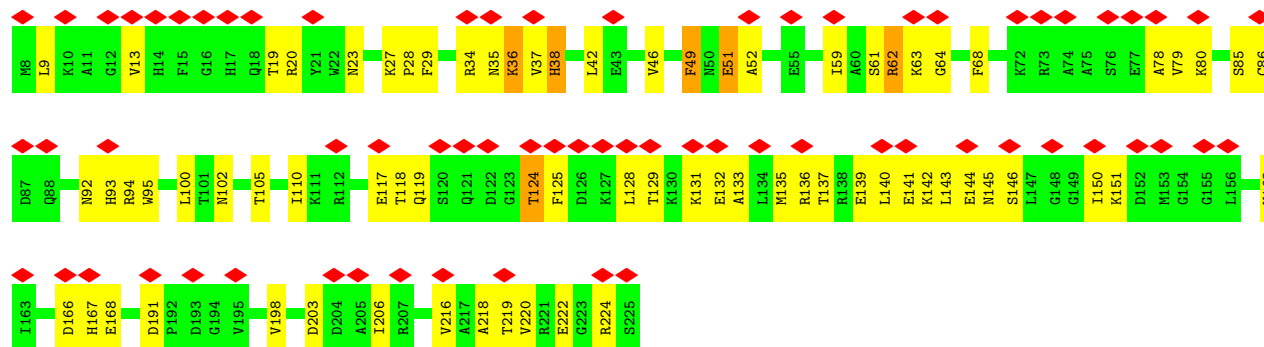


- Molecule 29: 16S ribosomal RNA



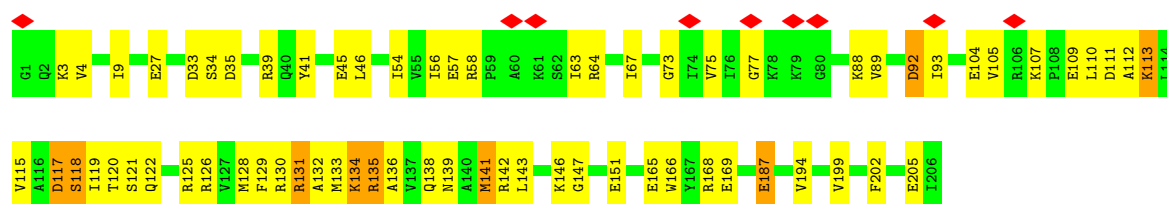


• Molecule 30: 30S ribosomal protein S2



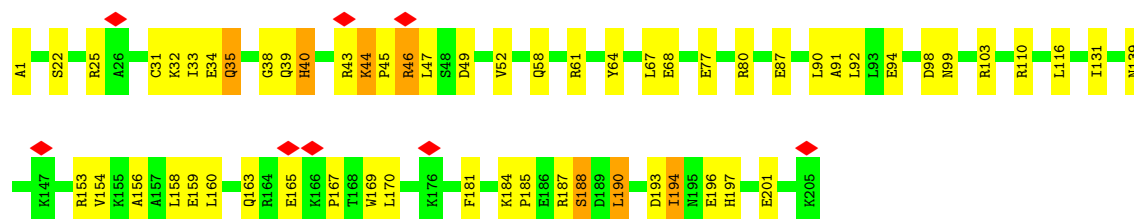
• Molecule 31: 30S ribosomal protein S3

Chain c: 



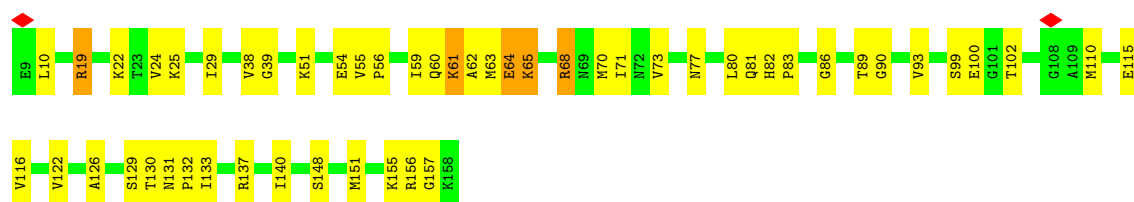
- Molecule 32: 30S ribosomal protein S4

Chain d: 



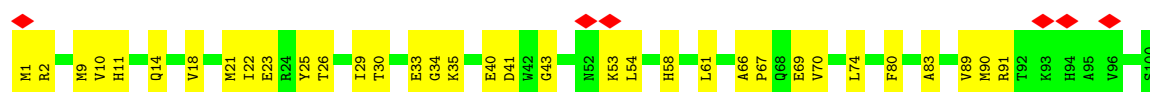
- Molecule 33: 30S ribosomal protein S5

Chain e: 



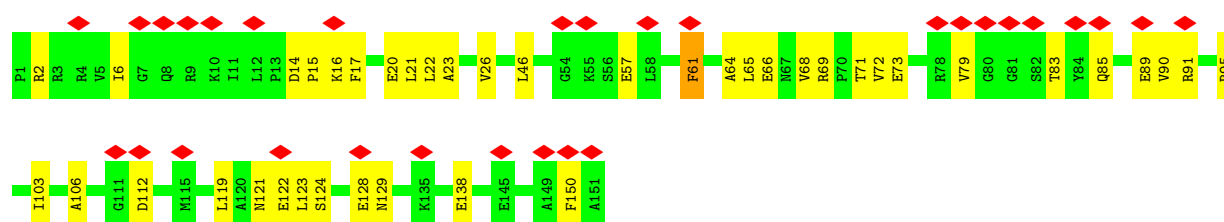
- Molecule 34: 30S ribosomal protein S6

Chain f: 



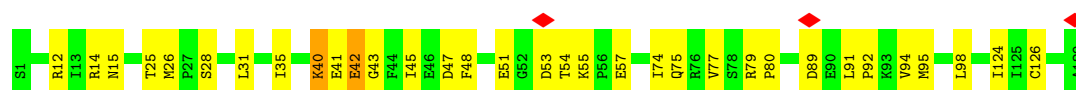
- Molecule 35: 30S ribosomal protein S7

Chain g: 



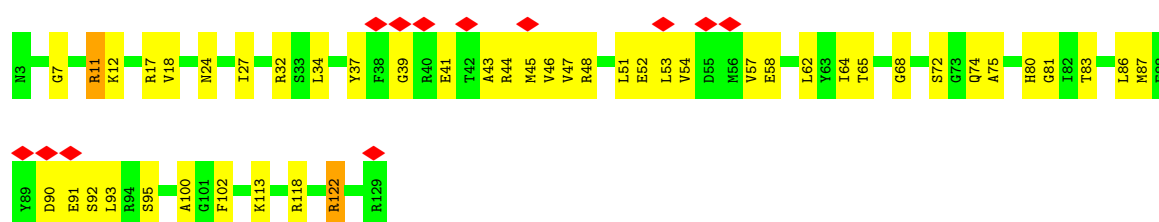
- Molecule 36: 30S ribosomal protein S8

Chain h: 



- Molecule 37: 30S ribosomal protein S9

Chain i: 



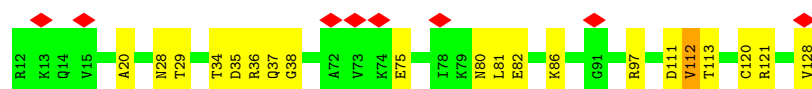
- Molecule 38: 30S ribosomal protein S10

Chain j: 



- Molecule 39: 30S ribosomal protein S11

Chain k: 



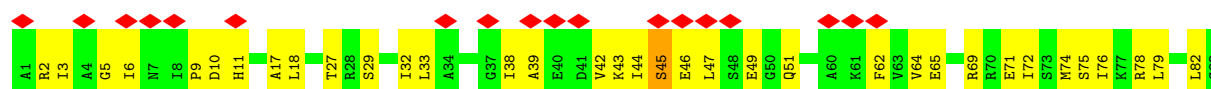
- Molecule 40: 30S ribosomal protein S12

Chain l: 



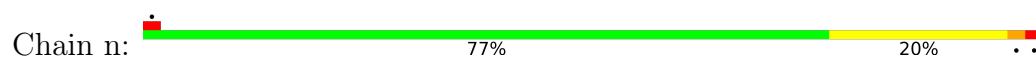
- Molecule 41: 30S ribosomal protein S13

Chain m: 

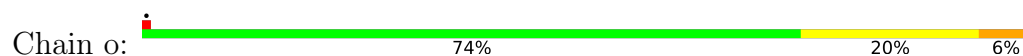




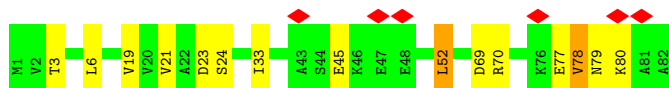
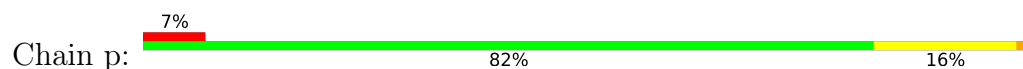
- Molecule 42: 30S ribosomal protein S14



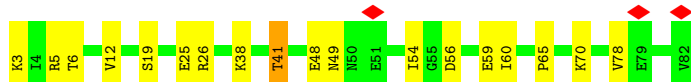
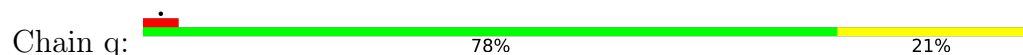
- Molecule 43: 30S ribosomal protein S15



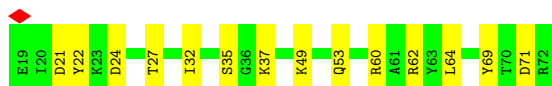
- Molecule 44: 30S ribosomal protein S16



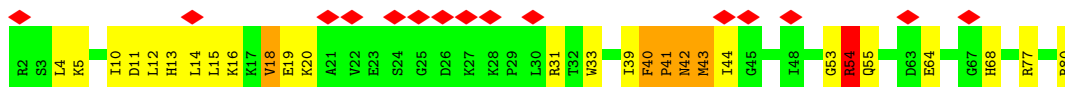
- Molecule 45: 30S ribosomal protein S17



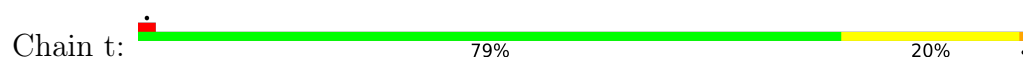
- Molecule 46: 30S ribosomal protein S18



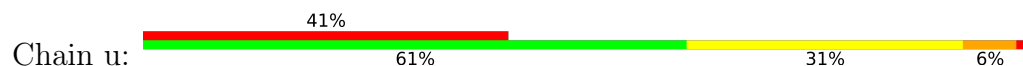
- Molecule 47: 30S ribosomal protein S19



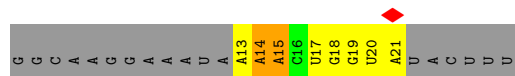
- Molecule 48: 30S ribosomal protein S20



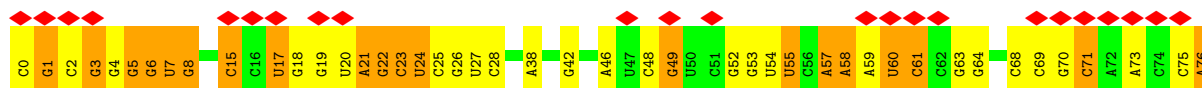
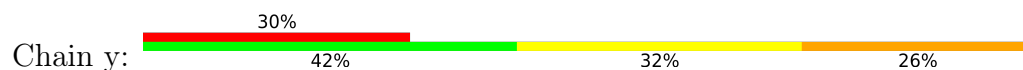
- Molecule 49: 30S ribosomal protein S21



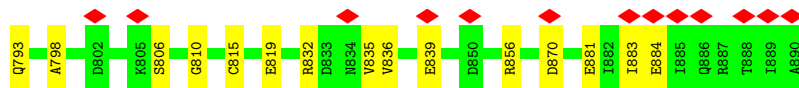
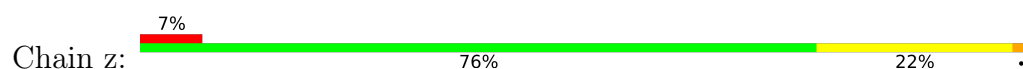
- Molecule 50: mRNA



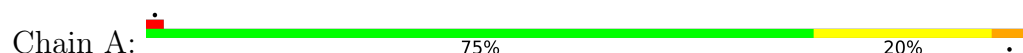
- Molecule 51: P-site tRNA-fMet M1

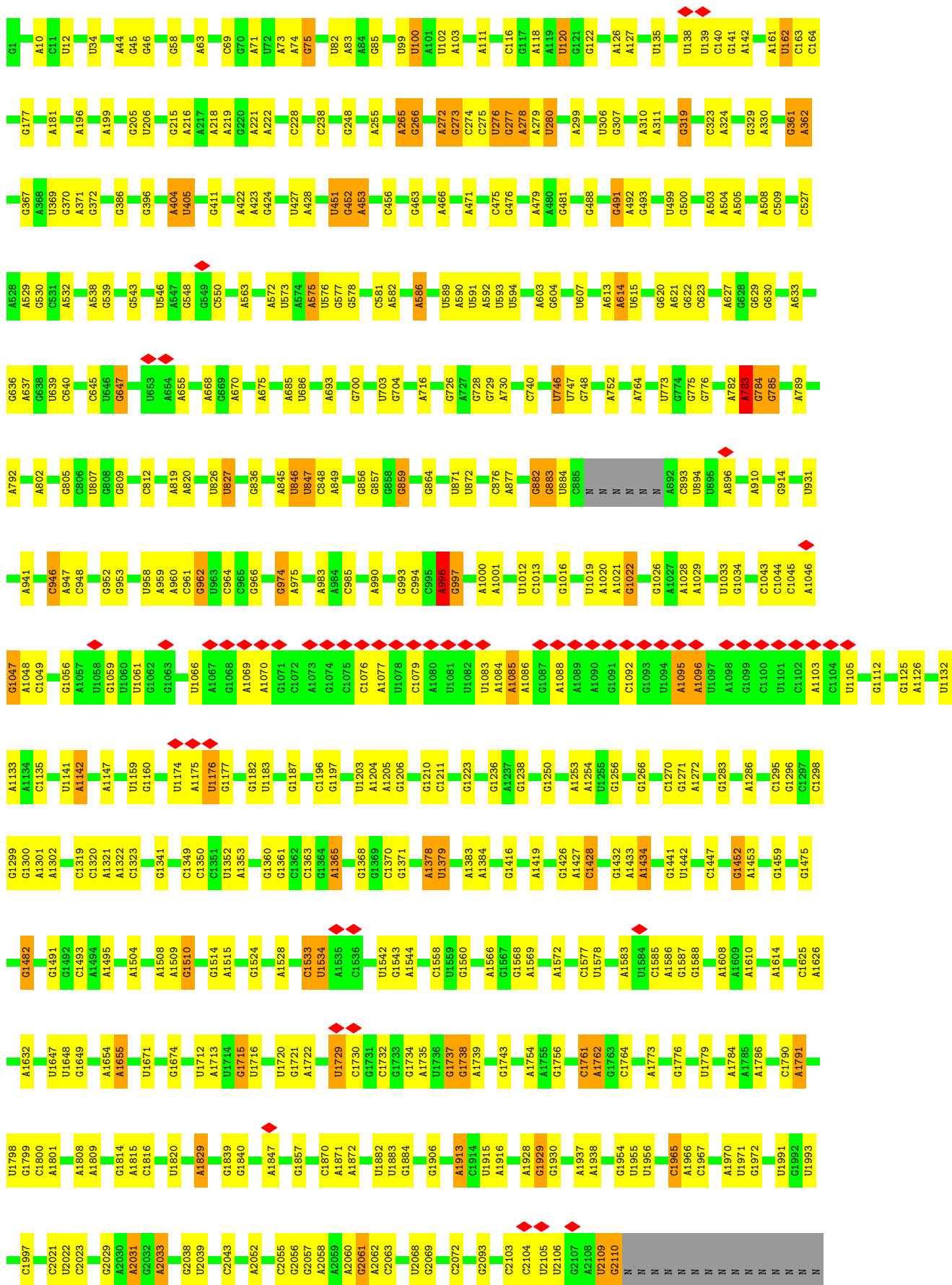


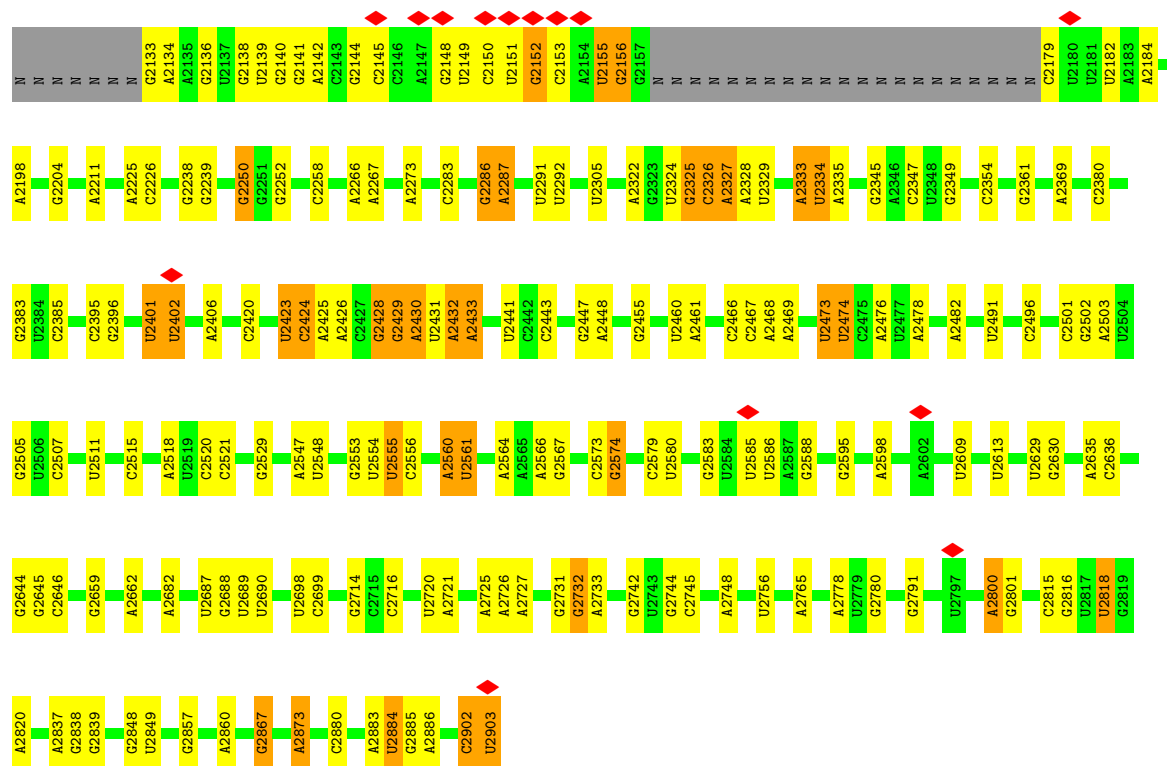
- Molecule 52: Translation initiation factor IF2



- Molecule 53: 23S ribosomal RNA







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	42825	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	28.167	Depositor
Minimum map value	-11.338	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.75	Depositor
Map size (Å)	416.768, 416.768, 416.768	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.814, 0.814, 0.814	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GCP, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	0	0.14	0/603	0.40	0/797
2	1	0.12	0/635	0.29	0/848
3	2	0.15	0/510	0.34	0/677
4	3	0.13	0/453	0.25	0/605
5	4	0.40	0/1586	0.44	1/2134 (0.0%)
6	5	0.37	0/450	0.39	0/599
7	6	0.11	0/417	0.26	0/554
8	7	0.14	0/380	0.29	0/498
9	8	0.09	0/513	0.26	0/676
10	9	0.19	0/2122	0.33	0/2852
11	E	0.30	0/1571	0.34	0/2113
12	F	0.20	0/1435	0.39	1/1926 (0.1%)
13	H	0.38	0/1343	0.50	2/1816 (0.1%)
14	J	0.21	0/1152	0.37	0/1551
15	K	0.14	0/948	0.32	0/1268
16	L	0.20	0/1054	0.39	0/1403
17	M	0.12	0/1093	0.28	0/1460
18	N	0.23	0/974	0.36	0/1301
19	O	0.12	0/902	0.30	0/1209
20	P	0.12	0/929	0.27	0/1242
21	Q	0.30	0/960	0.44	1/1278 (0.1%)
22	R	0.13	0/829	0.29	0/1107
23	S	0.56	1/864 (0.1%)	0.55	2/1156 (0.2%)
24	T	0.13	0/745	0.34	0/994
25	U	0.31	0/788	0.45	0/1051
26	V	0.14	0/766	0.35	0/1025
27	X	0.09	0/2825	0.22	0/4406
28	Y	0.17	0/303	0.33	0/397
29	a	0.13	0/36963	0.27	0/57662
30	b	0.24	0/1736	0.46	1/2338 (0.0%)
31	c	0.46	0/1652	0.49	0/2225
32	d	0.38	0/1665	0.52	2/2227 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.53	0/1119	0.54	1/1504 (0.1%)
34	f	0.17	0/836	0.39	0/1128
35	g	0.15	0/1196	0.34	0/1602
36	h	0.39	0/989	0.44	0/1326
37	i	0.24	0/1034	0.45	0/1375
38	j	0.12	0/797	0.33	0/1077
39	k	0.25	0/893	0.43	0/1205
40	l	0.31	1/969 (0.1%)	0.40	1/1300 (0.1%)
41	m	0.35	2/893 (0.2%)	0.41	0/1193
42	n	0.33	0/510	0.42	0/679
43	o	0.58	0/722	0.45	0/964
44	p	0.13	0/659	0.28	0/884
45	q	0.09	0/658	0.28	0/881
46	r	0.15	0/451	0.40	0/606
47	s	0.50	2/653 (0.3%)	0.61	0/877
48	t	0.29	0/671	0.43	2/888 (0.2%)
49	u	0.38	0/431	0.70	1/570 (0.2%)
50	x	0.39	0/217	0.59	0/336
51	y	0.15	0/1831	0.33	0/2853
52	z	0.36	0/3895	0.43	1/5264 (0.0%)
53	A	0.15	0/68614	0.29	7/107040 (0.0%)
All	All	0.20	6/157204 (0.0%)	0.32	23/234947 (0.0%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	s	53	GLY	C-N	8.37	1.44	1.33
23	S	96	ILE	C-N	8.34	1.45	1.33
47	s	54	ARG	C-N	-7.13	1.22	1.33
41	m	100	ARG	C-N	-6.81	1.23	1.33
41	m	99	GLN	C-N	-6.55	1.24	1.33

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	u	47	ALA	N-CA-C	-10.10	99.25	112.68
21	Q	49	ARG	N-CA-C	-10.02	100.31	112.54
23	S	96	ILE	CA-C-N	-7.76	112.44	122.77
23	S	96	ILE	C-N-CA	-7.76	112.44	122.77
30	b	51	GLU	N-CA-C	-7.57	103.03	112.72

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	596	0	610	22	0
2	1	625	0	655	8	0
3	2	509	0	543	14	0
4	3	449	0	491	4	0
5	4	1565	0	1616	29	0
6	5	444	0	461	3	0
7	6	410	0	440	5	0
8	7	377	0	418	2	0
9	8	504	0	574	4	0
10	9	2083	0	2157	30	0
11	E	1552	0	1619	34	0
12	F	1411	0	1447	43	0
13	H	1323	0	1374	38	0
14	J	1129	0	1162	27	0
15	K	939	0	1012	18	0
16	L	1045	0	1117	20	0
17	M	1074	0	1157	13	0
18	N	961	0	1000	6	0
19	O	892	0	923	15	0
20	P	917	0	965	11	0
21	Q	947	0	1022	26	0
22	R	816	0	839	13	0
23	S	857	0	922	5	0
24	T	739	0	807	12	0
25	U	780	0	834	15	0
26	V	753	0	780	18	0
27	X	2526	0	1282	17	0
28	Y	302	0	343	4	0
29	a	33012	0	16618	219	0
30	b	1705	0	1732	82	0
31	c	1625	0	1699	53	0
32	d	1643	0	1710	59	0
33	e	1106	0	1148	41	0
34	f	818	0	808	35	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	g	1182	0	1240	36	0
36	h	979	0	1034	26	0
37	i	1022	0	1070	66	0
38	j	787	0	828	20	0
39	k	877	0	887	16	0
40	l	955	0	1019	16	0
41	m	884	0	944	51	0
42	n	500	0	526	14	0
43	o	714	0	737	13	0
44	p	649	0	666	13	0
45	q	649	0	691	17	0
46	r	445	0	471	14	0
47	s	638	0	665	44	0
48	t	665	0	714	11	0
49	u	426	0	449	21	0
50	x	194	0	98	6	0
51	y	1639	0	837	29	0
52	z	3847	0	3911	107	0
53	A	61262	0	30823	326	0
54	A	201	0	0	0	0
54	a	85	0	0	0	0
54	z	1	0	0	0	0
55	z	32	0	14	2	0
All	All	145067	0	97909	1646	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1646 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:b:224:ARG:HD2	30:b:224:ARG:O	1.37	1.19
52:z:681:MET:HE1	52:z:686:VAL:CG1	1.74	1.16
41:m:3:ILE:CD1	41:m:44:ILE:HD11	1.78	1.13
52:z:789:GLU:O	52:z:789:GLU:OE1	1.63	1.13
52:z:681:MET:SD	52:z:686:VAL:HB	1.89	1.12

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	77/79 (98%)	59 (77%)	17 (22%)	1 (1%)	9	21
2	1	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
3	2	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
4	3	56/58 (97%)	53 (95%)	2 (4%)	1 (2%)	6	14
5	4	207/209 (99%)	187 (90%)	18 (9%)	2 (1%)	12	28
6	5	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
7	6	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
8	7	44/46 (96%)	42 (96%)	1 (2%)	1 (2%)	5	9
9	8	62/64 (97%)	60 (97%)	1 (2%)	1 (2%)	7	16
10	9	269/271 (99%)	249 (93%)	19 (7%)	1 (0%)	30	51
11	E	199/201 (99%)	183 (92%)	15 (8%)	1 (0%)	24	46
12	F	175/177 (99%)	157 (90%)	15 (9%)	3 (2%)	7	15
13	H	174/176 (99%)	148 (85%)	23 (13%)	3 (2%)	7	15
14	J	131/142 (92%)	117 (89%)	12 (9%)	2 (2%)	8	18
22	R	30/103 (29%)	27 (90%)	2 (7%)	1 (3%)	3	5
23	S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
24	T	91/93 (98%)	78 (86%)	12 (13%)	1 (1%)	11	25
25	U	100/102 (98%)	90 (90%)	9 (9%)	1 (1%)	12	28
26	V	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
28	Y	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	4	6
40	l	74/123 (60%)	70 (95%)	4 (5%)	0	100	100
41	m	112/114 (98%)	105 (94%)	7 (6%)	0	100	100
42	n	59/61 (97%)	48 (81%)	10 (17%)	1 (2%)	7	15
43	o	86/88 (98%)	79 (92%)	7 (8%)	0	100	100
44	p	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	9	21

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	q	78/80 (98%)	73 (94%)	5 (6%)	0	100	100
46	r	52/54 (96%)	50 (96%)	2 (4%)	0	100	100
47	s	77/79 (98%)	67 (87%)	8 (10%)	2 (3%)	4	7
48	t	83/85 (98%)	79 (95%)	3 (4%)	1 (1%)	10	23
49	u	49/51 (96%)	35 (71%)	12 (24%)	2 (4%)	2	3
52	z	188/509 (37%)	173 (92%)	14 (7%)	1 (0%)	24	46
All	All	3027/3535 (86%)	2743 (91%)	256 (8%)	28 (1%)	16	30

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	7	4	THR
12	F	139	GLU
25	U	92	VAL
28	Y	16	ILE
10	9	119	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	59/59 (100%)	59 (100%)	0	100	100
2	1	67/67 (100%)	67 (100%)	0	100	100
3	2	55/55 (100%)	52 (94%)	3 (6%)	19	41
4	3	48/48 (100%)	47 (98%)	1 (2%)	47	73
5	4	164/164 (100%)	162 (99%)	2 (1%)	63	83
6	5	47/47 (100%)	46 (98%)	1 (2%)	47	73
7	6	45/45 (100%)	45 (100%)	0	100	100
8	7	38/38 (100%)	38 (100%)	0	100	100
9	8	51/51 (100%)	51 (100%)	0	100	100
10	9	216/216 (100%)	212 (98%)	4 (2%)	50	75

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	E	165/165 (100%)	162 (98%)	3 (2%)	51	76
12	F	148/148 (100%)	145 (98%)	3 (2%)	48	74
13	H	137/137 (100%)	122 (89%)	15 (11%)	6	13
14	J	116/116 (100%)	115 (99%)	1 (1%)	70	87
15	K	103/103 (100%)	101 (98%)	2 (2%)	50	75
16	L	102/102 (100%)	99 (97%)	3 (3%)	37	65
17	M	109/109 (100%)	107 (98%)	2 (2%)	51	76
18	N	100/100 (100%)	100 (100%)	0	100	100
19	O	86/86 (100%)	85 (99%)	1 (1%)	63	83
20	P	99/99 (100%)	99 (100%)	0	100	100
21	Q	89/89 (100%)	89 (100%)	0	100	100
22	R	84/84 (100%)	83 (99%)	1 (1%)	63	83
23	S	93/93 (100%)	90 (97%)	3 (3%)	34	62
24	T	80/80 (100%)	79 (99%)	1 (1%)	61	82
25	U	83/83 (100%)	80 (96%)	3 (4%)	31	58
26	V	78/78 (100%)	78 (100%)	0	100	100
28	Y	34/34 (100%)	34 (100%)	0	100	100
30	b	180/180 (100%)	175 (97%)	5 (3%)	38	66
31	c	170/170 (100%)	158 (93%)	12 (7%)	13	31
32	d	172/172 (100%)	165 (96%)	7 (4%)	27	54
33	e	113/113 (100%)	101 (89%)	12 (11%)	6	14
34	f	87/87 (100%)	87 (100%)	0	100	100
35	g	124/124 (100%)	121 (98%)	3 (2%)	43	70
36	h	104/104 (100%)	99 (95%)	5 (5%)	23	47
37	i	105/105 (100%)	102 (97%)	3 (3%)	37	65
38	j	86/86 (100%)	86 (100%)	0	100	100
39	k	90/90 (100%)	88 (98%)	2 (2%)	45	72
40	l	103/103 (100%)	101 (98%)	2 (2%)	50	75
41	m	92/92 (100%)	90 (98%)	2 (2%)	45	72
42	n	52/52 (100%)	50 (96%)	2 (4%)	29	56
43	o	76/76 (100%)	67 (88%)	9 (12%)	5	10

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	p	65/65 (100%)	62 (95%)	3 (5%)	24	49
45	q	74/74 (100%)	72 (97%)	2 (3%)	39	67
46	r	47/47 (100%)	47 (100%)	0	100	100
47	s	70/70 (100%)	65 (93%)	5 (7%)	13	31
48	t	65/65 (100%)	63 (97%)	2 (3%)	35	63
49	u	44/44 (100%)	40 (91%)	4 (9%)	9	19
52	z	409/409 (100%)	383 (94%)	26 (6%)	16	35
All	All	4824/4824 (100%)	4669 (97%)	155 (3%)	35	62

5 of 155 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	p	78	VAL
52	z	436	GLU
47	s	40	PHE
52	z	405	THR
52	z	663	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
24	T	59	ASN
32	d	130	ASN
52	z	498	ASN
24	T	91	GLN
31	c	99	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	X	117/118 (99%)	10 (8%)	0
29	a	1538/1539 (99%)	200 (13%)	0
50	x	8/27 (29%)	3 (37%)	0
51	y	76/77 (98%)	25 (32%)	0
53	A	2850/2903 (98%)	352 (12%)	31 (1%)
All	All	4589/4664 (98%)	590 (12%)	31 (0%)

5 of 590 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
27	X	15	A
27	X	35	C
27	X	44	G
27	X	87	U
27	X	88	C

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
53	A	882	G
53	A	2432	A
53	A	1095	A
53	A	2560	A
53	A	2401	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 288 ligands modelled in this entry, 287 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
55	GCP	z	2001	54	32,34,34	1.14	3 (9%)	49,54,54	1.92	13 (26%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	GCP	z	2001	54	-	4/19/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	z	2001	GCP	PG-O3G	2.39	1.60	1.55
55	z	2001	GCP	C6-N1	-2.28	1.34	1.38
55	z	2001	GCP	PG-O2G	2.25	1.60	1.55

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	z	2001	GCP	PB-O3A-PA	-6.60	110.82	132.37
55	z	2001	GCP	C5-C4-N3	-5.16	120.18	128.39
55	z	2001	GCP	C2-N3-C4	4.91	120.76	112.30
55	z	2001	GCP	N9-C4-N3	3.88	133.71	125.95
55	z	2001	GCP	C8-N7-C5	2.78	109.21	104.26

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	z	2001	GCP	PB-C3B-PG-O1G
55	z	2001	GCP	PB-C3B-PG-O2G
55	z	2001	GCP	PB-C3B-PG-O3G
55	z	2001	GCP	PG-C3B-PB-O2B

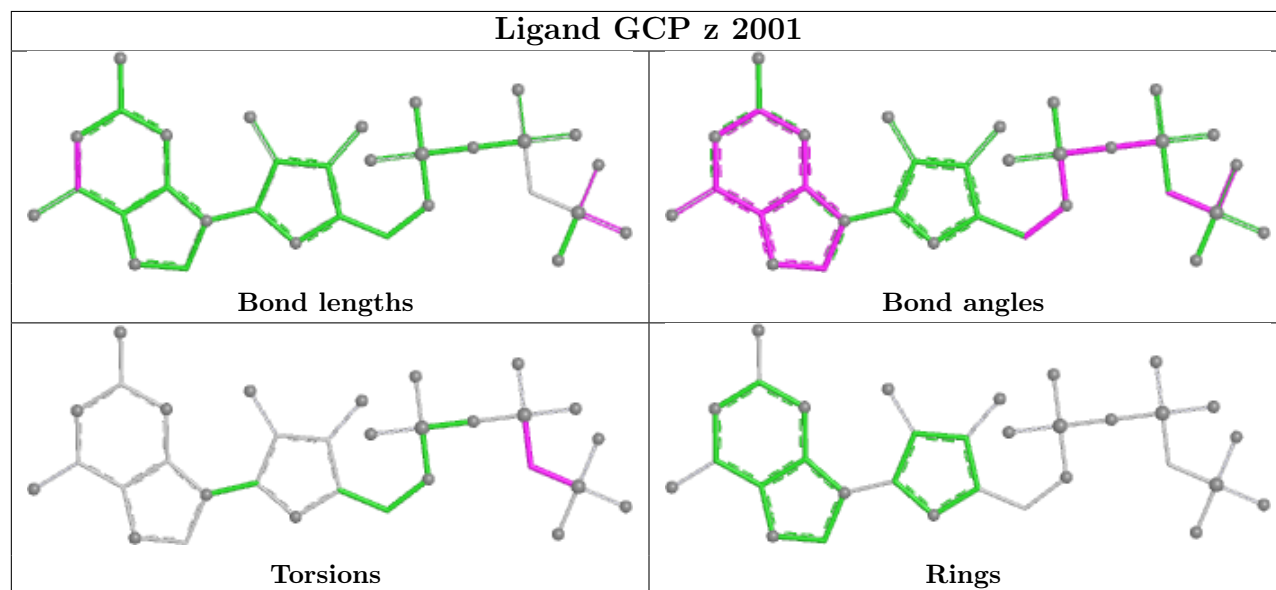
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
55	z	2001	GCP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

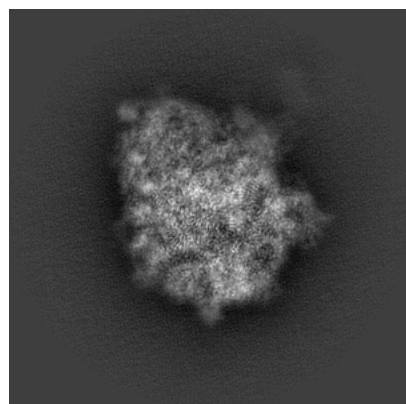
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43930. These allow visual inspection of the internal detail of the map and identification of artifacts.

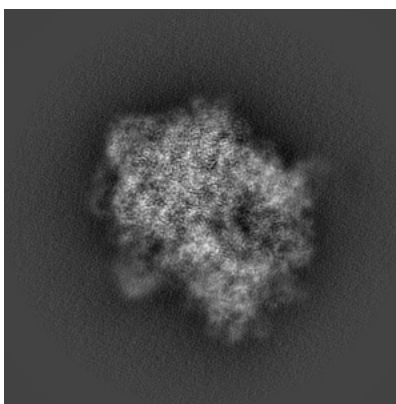
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

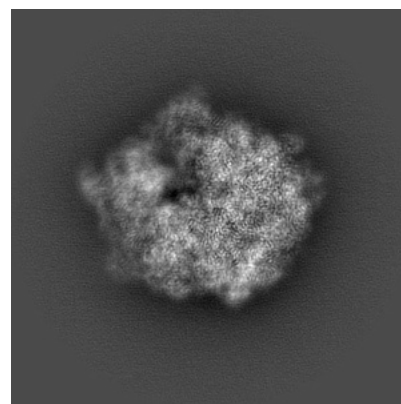
6.1.1 Primary map



X

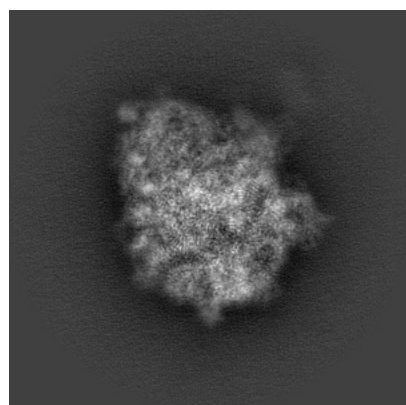


Y

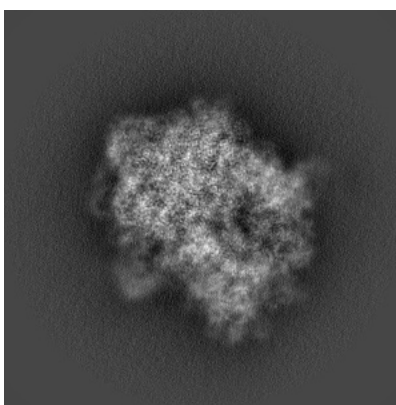


Z

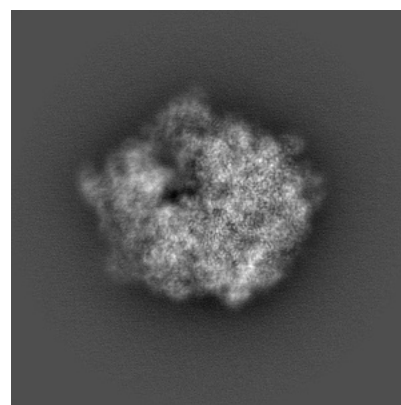
6.1.2 Raw map



X



Y

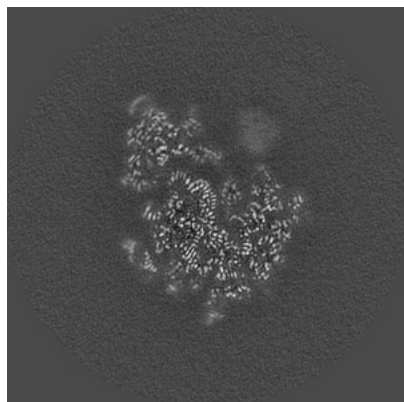


Z

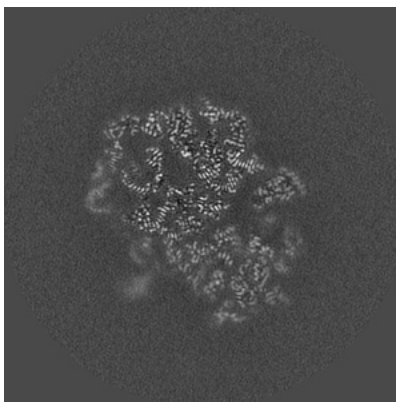
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

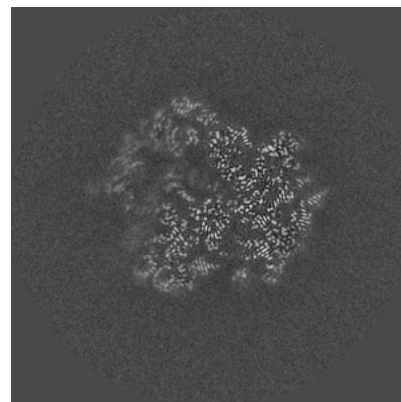
6.2.1 Primary map



X Index: 256

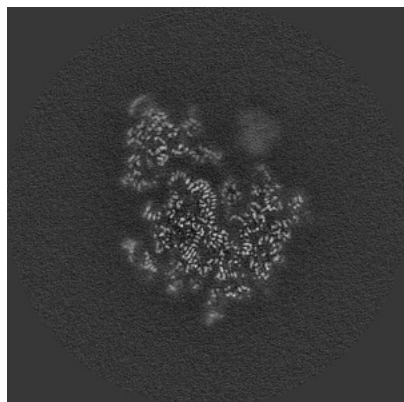


Y Index: 256

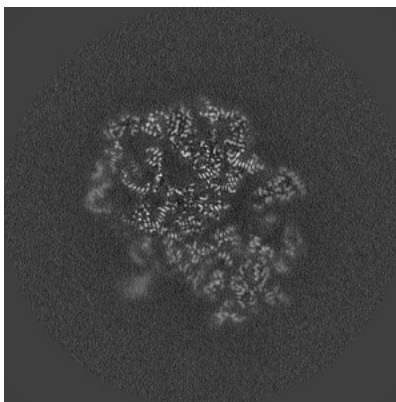


Z Index: 256

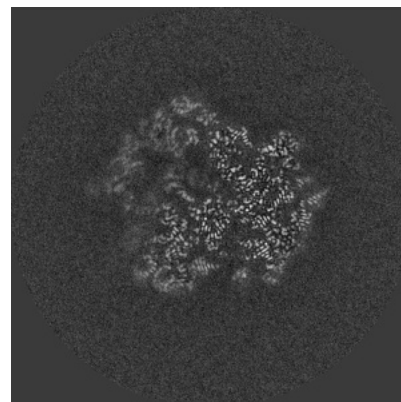
6.2.2 Raw map



X Index: 256



Y Index: 256

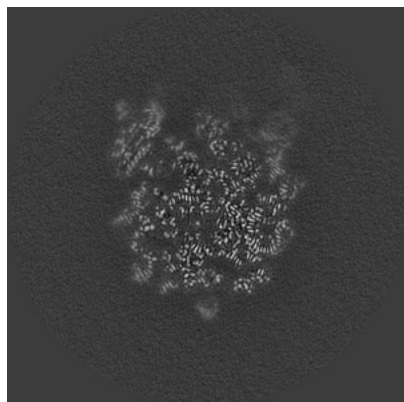


Z Index: 256

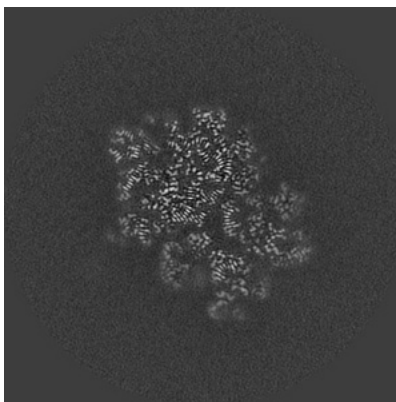
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

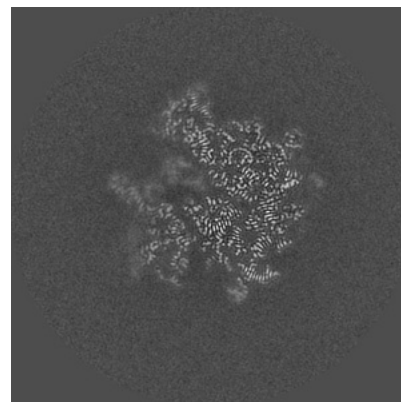
6.3.1 Primary map



X Index: 296

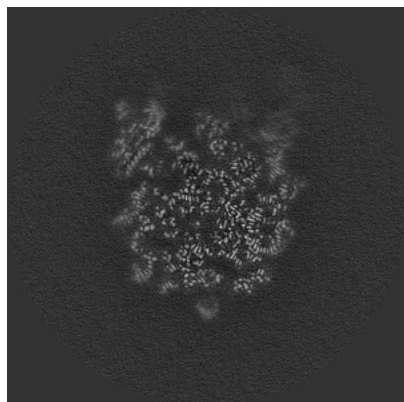


Y Index: 233

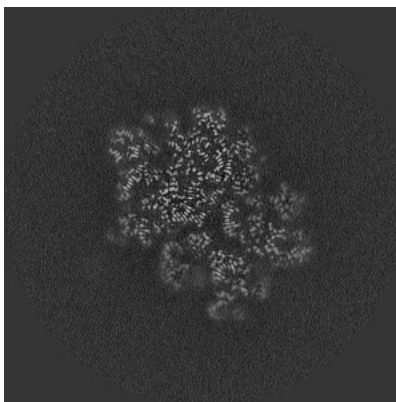


Z Index: 238

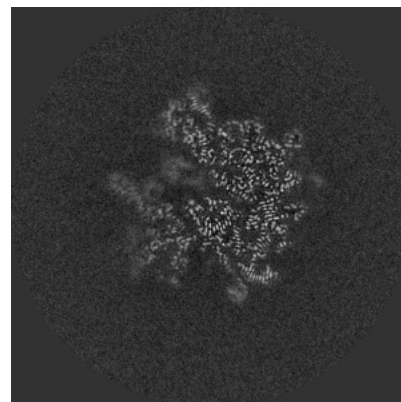
6.3.2 Raw map



X Index: 296



Y Index: 233

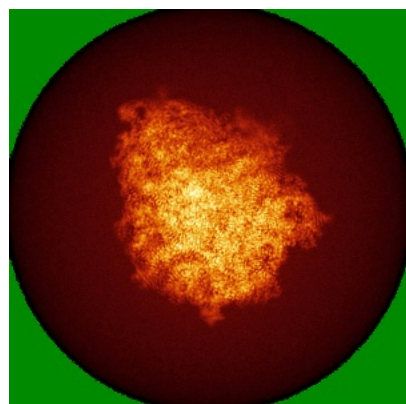


Z Index: 237

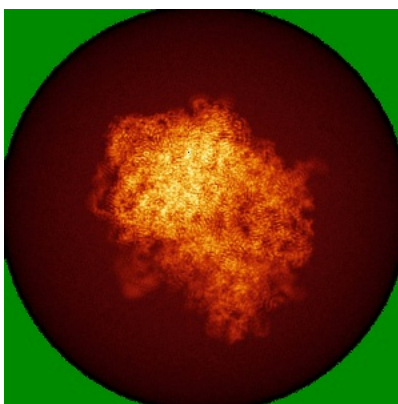
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

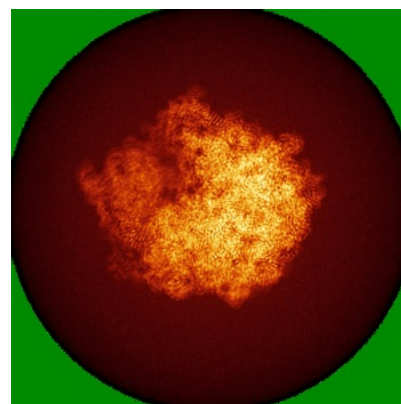
6.4.1 Primary map



X

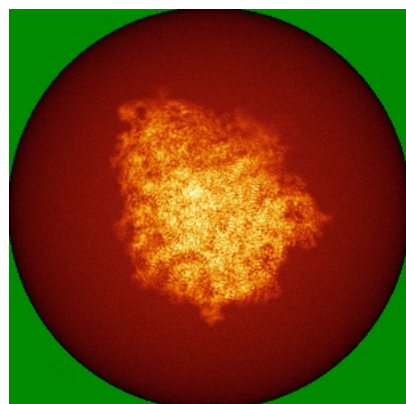


Y

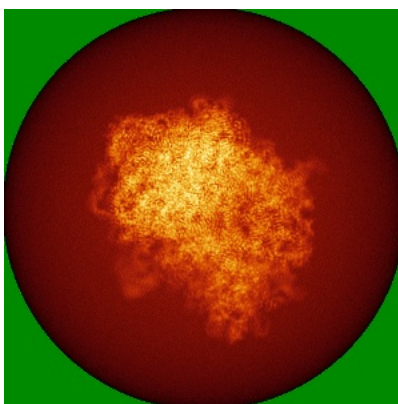


Z

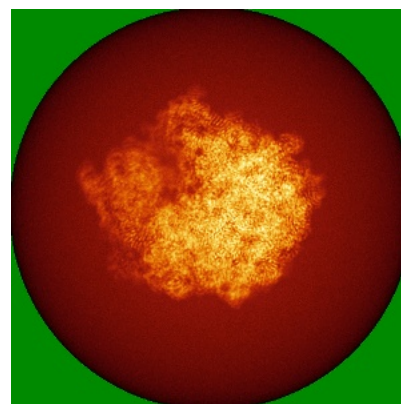
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

This section was not generated.

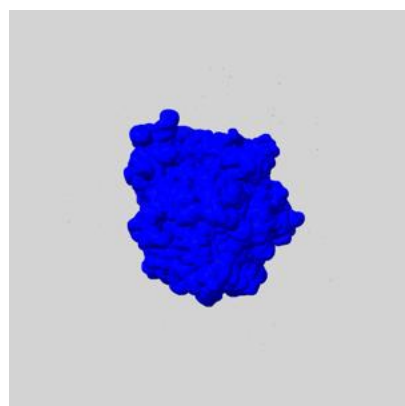
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

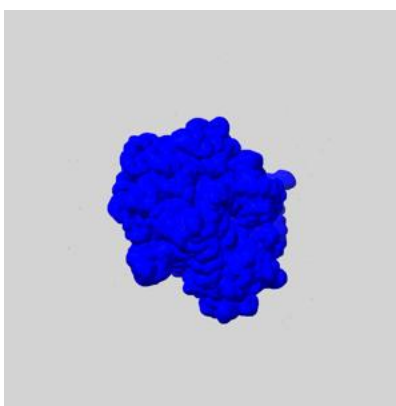
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

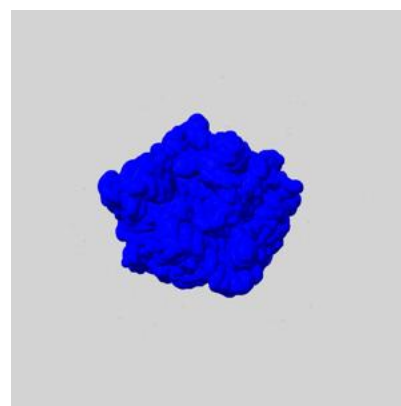
6.6.1 emd_43930_msk_1.map [i](#)



X



Y

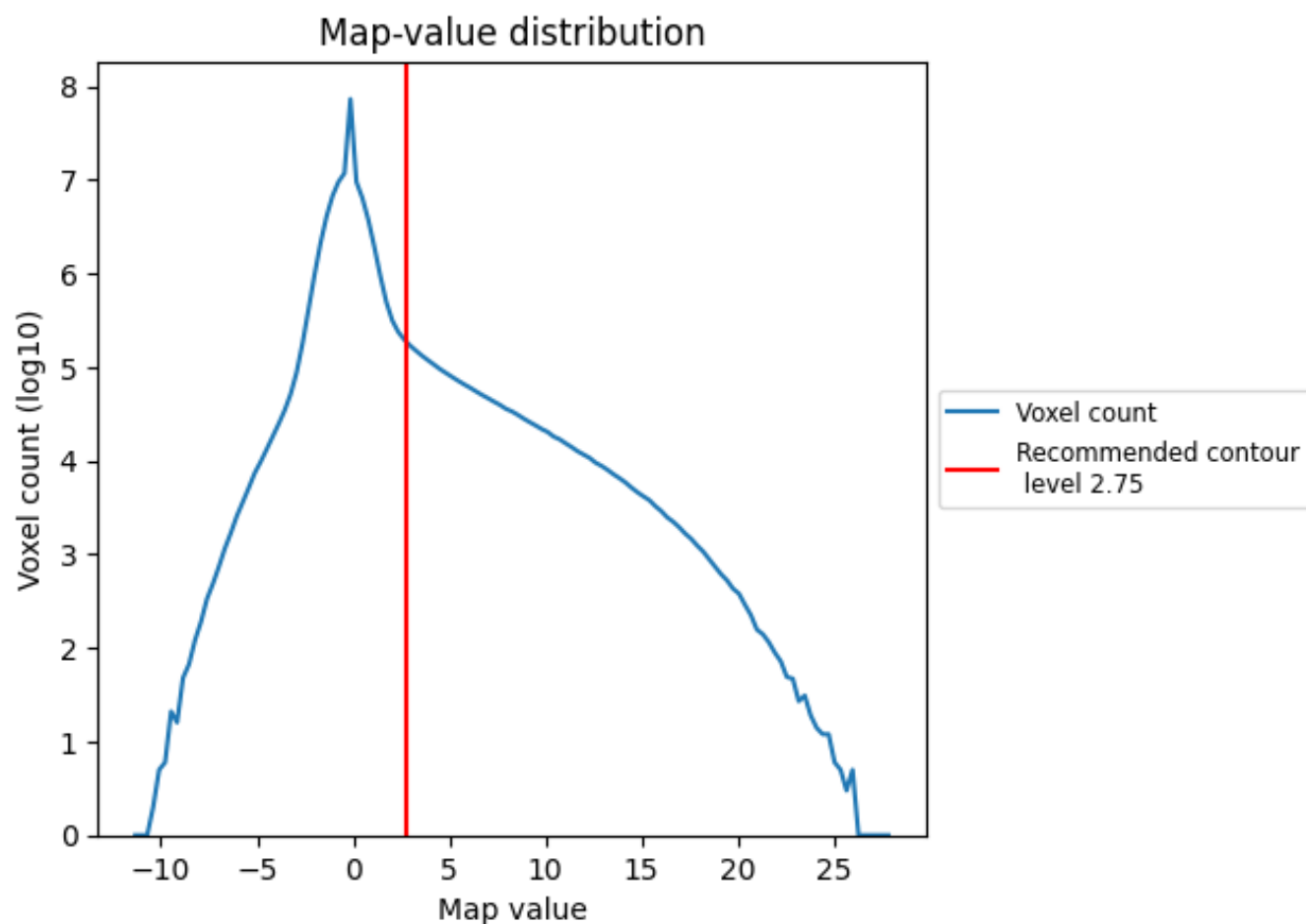


Z

7 Map analysis [i](#)

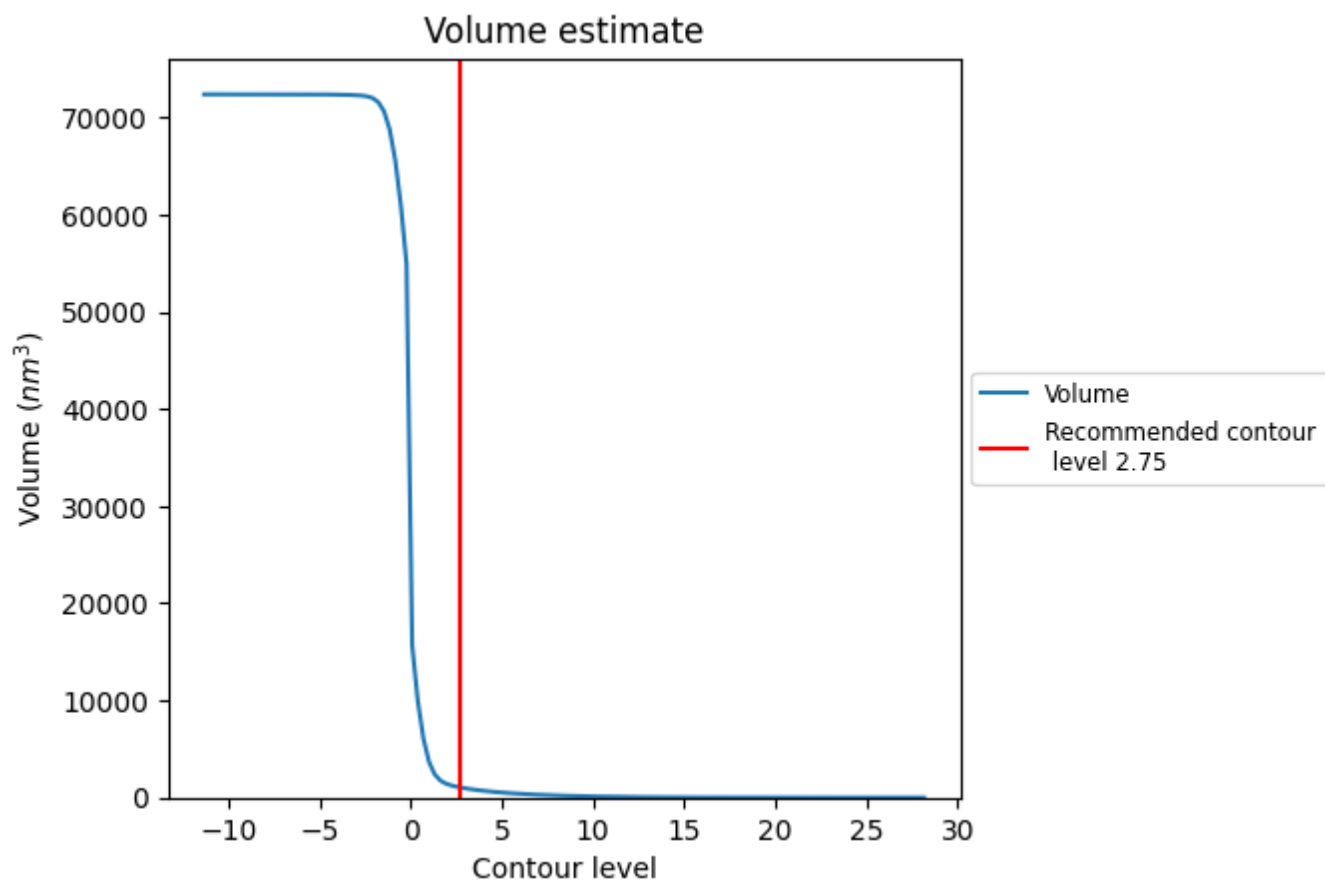
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

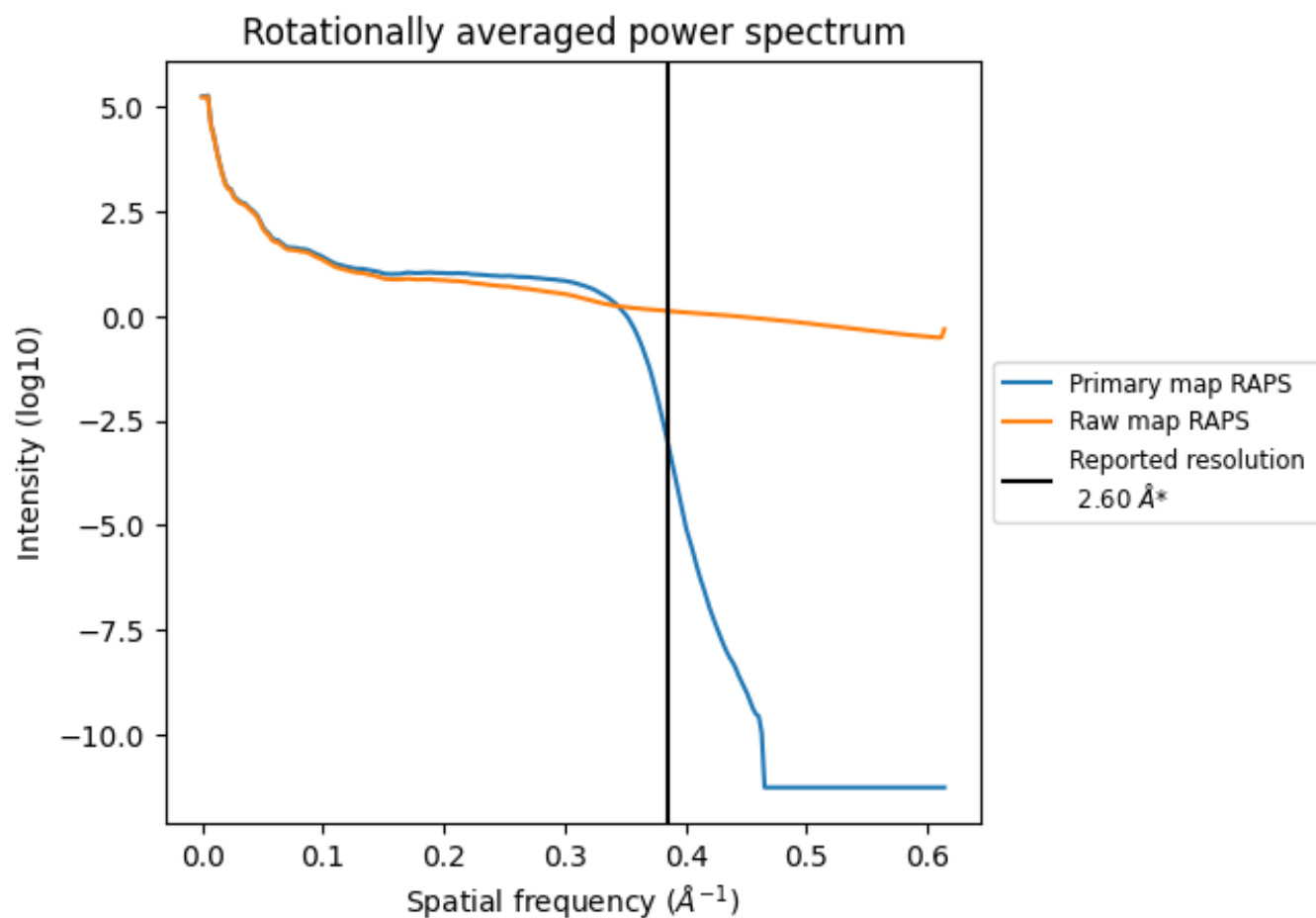
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1031 nm³; this corresponds to an approximate mass of 931 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

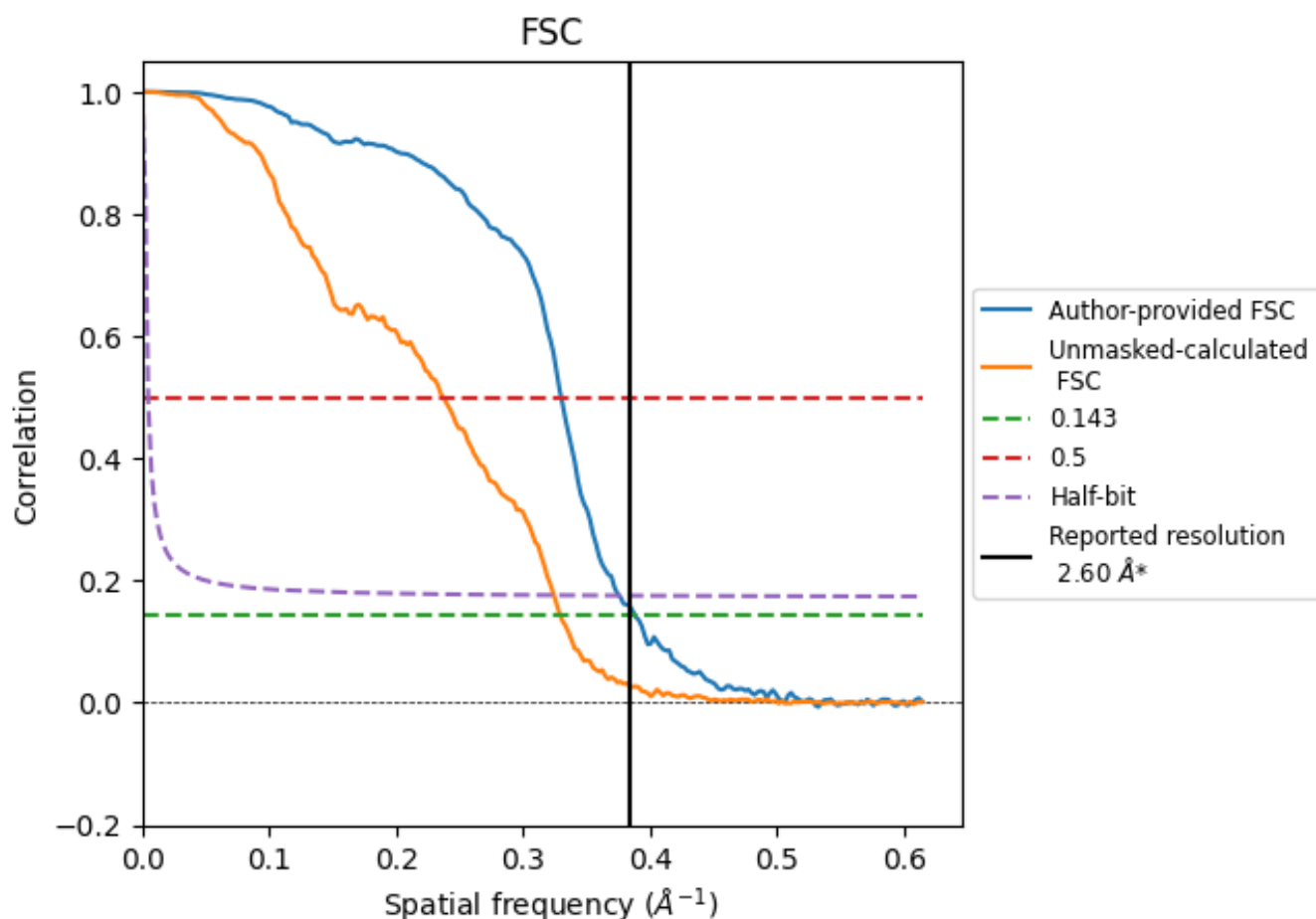


*Reported resolution corresponds to spatial frequency of 0.385 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.385 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.60	-	-
Author-provided FSC curve	2.58	3.03	2.66
Unmasked-calculated*	3.04	4.22	3.08

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.04 differs from the reported value 2.6 by more than 10 %

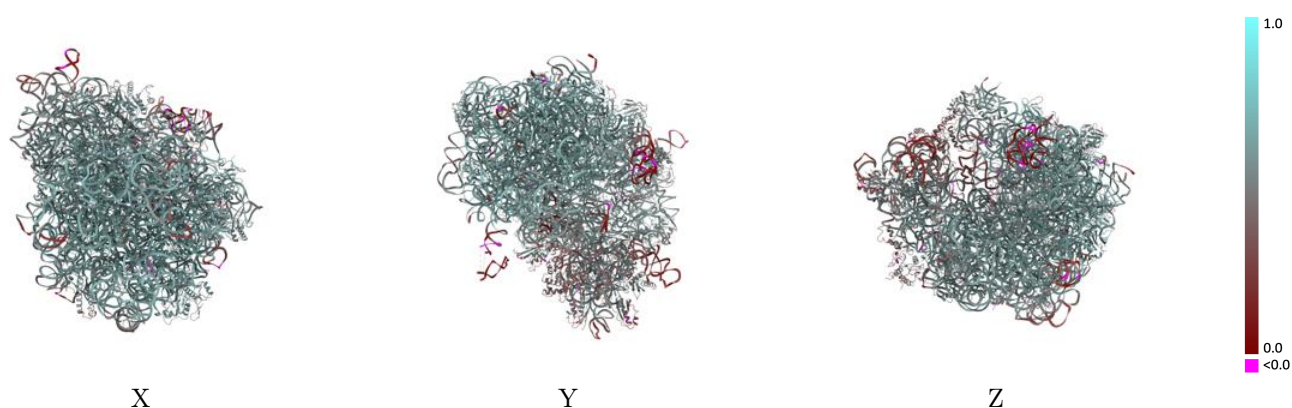
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43930 and PDB model 9AX8. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)

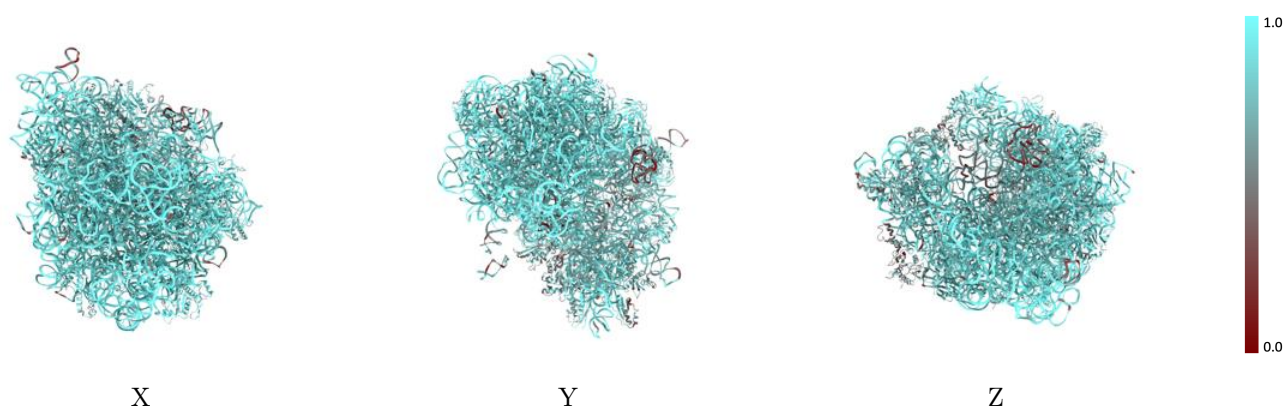
This section was not generated.

9.2 Q-score mapped to coordinate model [i](#)



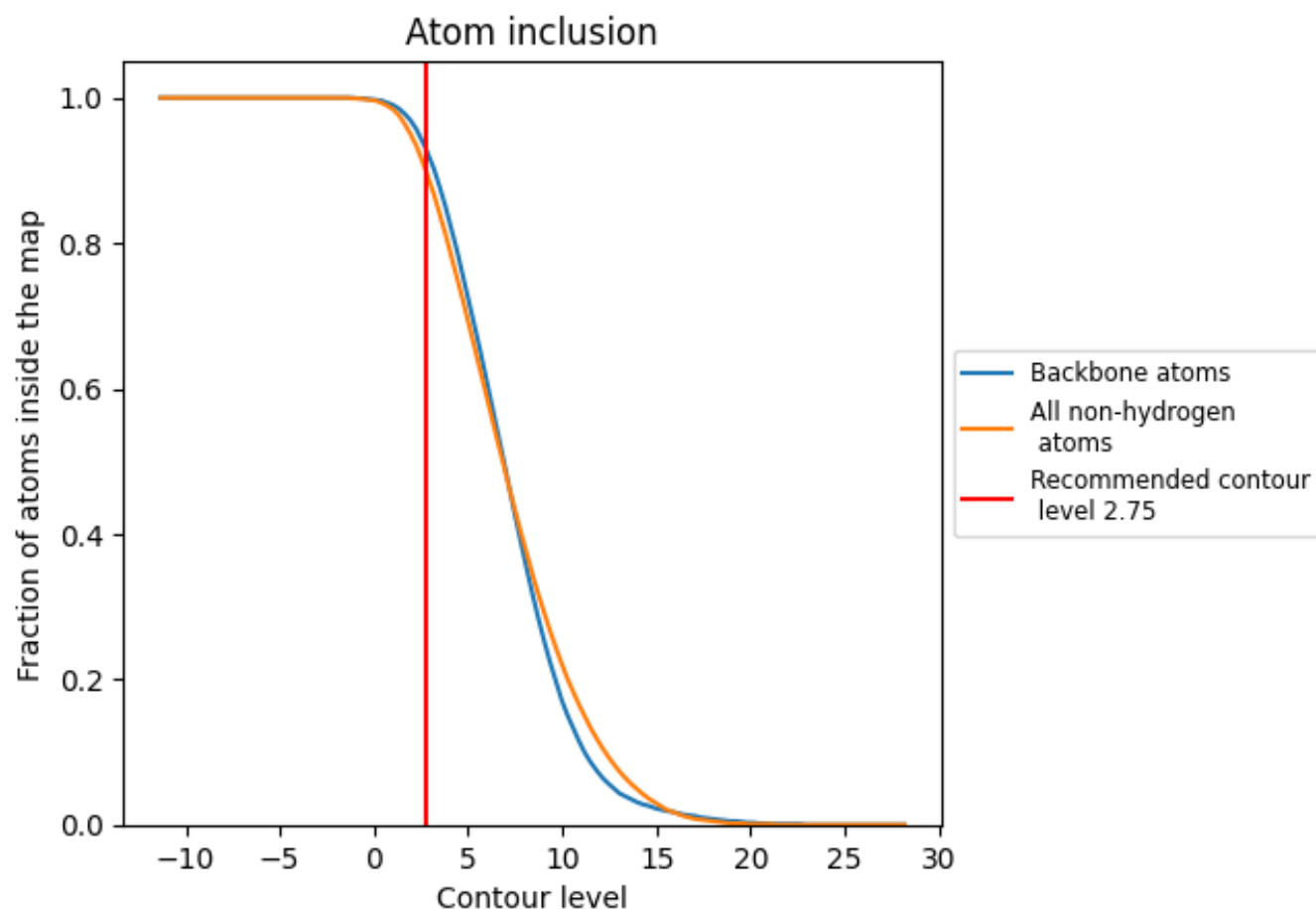
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.75).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (2.75) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9000	 0.5520
0	 0.7170	 0.4190
1	 0.8980	 0.5950
2	 0.8130	 0.4840
3	 0.8900	 0.5910
4	 0.9020	 0.5810
5	 0.8950	 0.5980
6	 0.8310	 0.5740
7	 0.9180	 0.6190
8	 0.9410	 0.6360
9	 0.9050	 0.6070
A	 0.9550	 0.5860
E	 0.8880	 0.5740
F	 0.6810	 0.4260
H	 0.8260	 0.5310
J	 0.8970	 0.5770
K	 0.8760	 0.5940
L	 0.8930	 0.5660
M	 0.8920	 0.6050
N	 0.9430	 0.6110
O	 0.8920	 0.5500
P	 0.8660	 0.5810
Q	 0.9340	 0.6070
R	 0.8820	 0.5600
S	 0.8850	 0.6000
T	 0.8240	 0.5310
U	 0.8460	 0.5310
V	 0.8730	 0.5820
X	 0.9740	 0.5700
Y	 0.8630	 0.5840
a	 0.9380	 0.5360
b	 0.5040	 0.3920
c	 0.7540	 0.5150
d	 0.7970	 0.5090
e	 0.8580	 0.5530



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
f	 0.7490	 0.4590
g	 0.6090	 0.3920
h	 0.8480	 0.5640
i	 0.7090	 0.4130
j	 0.7030	 0.4380
k	 0.7610	 0.4880
l	 0.8000	 0.5440
m	 0.6410	 0.3880
n	 0.7840	 0.4740
o	 0.8620	 0.5590
p	 0.8360	 0.5400
q	 0.8180	 0.5280
r	 0.8380	 0.5470
s	 0.6080	 0.3740
t	 0.8540	 0.5450
u	 0.4860	 0.2240
x	 0.6860	 0.5520
y	 0.5690	 0.3010
z	 0.7430	 0.5270